AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the application.

1.-16. (Cancelled)

17. (Currently Amended) A method of immunizing an animal, which method comprises:

(a) administering an isolated nucleic acid encoding an infectious attenuated Kunjin virus to an animal, and

(b) ~~thereby~~ eliciting a protective immune response to a West Nile Virus in the animal.

18. (Original) The method of claim 17, wherein the isolated nucleic acid corresponds to substantially an entire genome of a Kunjin virus.

19. (Previously Presented) The method of claim 18, wherein the isolated nucleic acid encodes at least one attenuating mutation.

20. (Previously Presented) The method of claim 19, wherein the isolated nucleic acid is DNA operably linked to a promoter operable in a mammalian cell.

21. (Original) The method of claim 19, wherein the isolated nucleic acid is RNA.

22. (Original) The method of claim 21, wherein the RNA is packaged in virions.

23. (Cancelled)

24. (Cancelled)

25. (Previously Presented) The method of claim 17, wherein the West Nile virus is NY99 strain West Nile virus.

26. (Original) The method of claim 17, wherein the animal is a mammal.

27. (Original) The method of claim 26, wherein the mammal is an equine.

28. (Original) The method of claim 26, wherein the mammal is a human.

29. (Original) The method of claim 17, wherein the animal is an avian.

30.-37. (Cancelled)

38. (Currently Amended) A method of inducing an immune response in an animal, which method comprises:

(a) administering an isolated nucleic acid encoding an infectious attenuated Kunjin virus comprising at least one attenuating mutation to an animal, and

(b) ~~thereby~~ eliciting an immune response to at least another flavivirus in the animal.

39. (Previously Presented) The method of claim 38, wherein the isolated nucleic acid corresponds to substantially an entire genome of a Kunjin virus.

40. (Cancelled)

41. (Previously Presented) The method of claim 38, wherein the isolated nucleic acid is DNA operably linked to a promoter operable in a mammalian cell.

42. (Previously Presented) The method of claim 38, wherein the isolated nucleic acid is RNA.

43. (Previously Presented) The method of claim 42, wherein the RNA is packaged into virions.

44. (Previously Presented) The method of claim 38, wherein the at least another flavivirus is more pathogenic than Kunjin virus.

45. (Previously Presented) The method of claim 44, wherein the at least another flavivirus is a West Nile virus.

46. (Previously Presented) The method of claim 45, wherein the West Nile virus is NY99 strain West Nile virus.

47. (Previously Presented) The method of claim 38, wherein the animal is a mammal.

48. (Previously Presented) The method of claim 47, wherein the mammal is an equine.

49. (Previously Presented) The method of claim 47, wherein the mammal is a human.

50. (Previously Presented) The method of claim 38, wherein the animal is an avian.

51. (Previously Presented) The method of claim 19, wherein the isolated nucleic acid encodes at least one attenuating mutation in a Kunjin virus non-structural protein.

52. (Previously Presented) The method of claim 51, wherein the attenuating mutation is located at an amino acid residue selected from the group consisting of proline residue 250 of nonstructural protein NS1, alanine residue 30 of nonstructural protein NS2A, asparagine residue 101 of nonstructural protein NS2A, and proline residue 270 of nonstructural protein NS5.

53. (Previously Presented) The method of claim 52, wherein the attenuating mutation is selected from the group consisting of proline residue 250 of nonstructural protein NS1 substituted by leucine, valine, or alanine, alanine residue 30 of nonstructural protein NS2A substituted by proline, asparagine residue 101 of nonstructural protein NS2A substituted by aspartate, and proline residue 270 of nonstructural protein NS5 substituted by serine.

54. (Withdrawn) The method of claim 19, wherein the isolated nucleic acid encodes at least one attenuating mutation in a Kunjin virus structural protein.

55. (Withdrawn) The method of claim 54, wherein the Kunjin virus structural protein is E protein.

56. (Withdrawn) The method of claim 55, wherein the attenuating mutation is located at an amino acid residue selected from the group consisting of residue 49, residue 138, residue 306, and residue 390 of E protein.

57. (Withdrawn) The method of claim 56, wherein the attenuating mutation is glutamate residue 390 of E protein substituted by glycine.

58. (Previously Presented) The method of claim 38, wherein the attenuating mutation is located in a Kunjin-virus non-structural protein.

59. (Previously Presented) The method of claim 58, wherein the attenuating mutation is located at an amino acid residue selected from the group consisting of proline residue 250 of nonstructural protein NS1, alanine residue 30 of nonstructural protein NS2A, asparagine residue 101 of nonstructural protein NS2A, and proline residue 270 of nonstructural protein NS5.

60. (Previously Presented) The method of claim 59, wherein the attenuating mutation is selected from the group consisting of proline residue 250 of nonstructural protein NS1 substituted by leucine, valine, or alanine, alanine residue 30 of nonstructural protein NS2A substituted by proline, asparagine residue 101 of nonstructural protein NS2A substituted by aspartate, and proline residue 270 of nonstructural protein NS5 substituted by serine.

61. (Withdrawn) The method of claim 38, wherein the attenuating mutation is located in a Kunjin virus structural protein.

62. (Withdrawn) The method of claim 61, wherein the Kunjin virus structural protein is E protein.

63. (Withdrawn) The method of claim 62, wherein the attenuating mutation is located at an amino acid residue selected from the group consisting of residue 49, residue 138, residue 306, and residue 390 of E protein.

64. (Withdrawn) The method of claim 63, wherein the attenuating mutation is glutamate residue 390 of E protein substituted by glycine.